Amendments to the Specification:

At page 1, delete the paragraph, spanning lines 12-14.

At page 1, line 6, insert the following paragraph.

Cross-Reference to Related Applications

This application is a continuation-in-part of U.S. Serial No. 09/827,789 filed on April 6, 2001 which, in turn, claims benefit of U.S. provisional application 60/195,097, filed on April 6, 2000.

At page 12, replace the fourth paragraph, beginning at line 29, and continuing on page 13, with the following paragraph.

For *esp-2* and *esp-8* mutants we have utilized the recently developed mapping strain CB4856 that contains a large number of single nucleotide polymorphisms or SNPs (Wicks et al., *WBG* 16(1): 28; see also the *C. elegans* SNP index at the Genome Sequencing Center website at Washington University at St. Louis ~~http://genome.wustl.edu/gsc/C_elegans/SNP/index.html~~). Many snip-SNP markers, that are detected by a restriction digest, have been identified from CB4856. CB4856 has several advantages over RW7000 as a mapping strain, there are more SNP markers than TC1 markers for use in mapping and the SNP markers permit the detection of both the CB4856 and the N2 allele. We crossed CB4856 males to *esp-2* and picked approximately 1,000 F2 hermaphrodite cross progeny directly to SKA plates. After 24 hours on PA14 SKA plates, over 200 dead animals were singly placed onto *E. coli* plates, with the assumption that these would be *esp-2/esp-2* animals. 130 of the dead animals yielded progeny. The *esp-2/esp-2* plates were allowed to starve, the worms were washed from the plate, and DNA was prepared from these worms according to standard methods. All of the original plates were saved, so that it was then possible to verify the Esp phenotype of each F2 picked (this was done for 20% of the strains, all critical recombinants were rigorously tested for their Esp phenotype).